

Figure 1A

1 CCCACGCGTCCGGGGAGCTTGCACTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC 60  
 61 CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTTCATAAAATATAATTTGCTC 120  
 121 TTTCACTTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA 180  
 181 GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG 240  
 241 CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC 300  
 301 TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT 360  
 361 AAGGGAAAAC TAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT 420  
 421 GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAAC TGAGCATGGAGAGAAAAATT 480  
 481 TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA 540  
 1 M E P N G T F S N 9  
 541 TAACAACAGCAGGAAC TGACAATTGAAAACTTCAAGAGAGAATTTTCCCAATTGTATA 600  
 10 N N S R N C T I E N F K R E F F P I V Y 29  
 601 TCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTCTCTGCA 660  
 30 L I I F F W G V L G N G L S I Y V F L Q 49  
 661 GCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTGGCCATTCAGATCT 720  
 50 P Y K K S T S V N V F M L N L A I S D L 69  
 721 CCTGTTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT 780  
 70 L F I S T L P F R A D Y Y L R G S N W I 89  
 781 ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCTTGTATGTCAACATGTACAGCAG 840  
 90 F G D L A C R I M S Y S L Y V N M Y S S 109  
 841 TATTTATTTCTGACCGTGCTGAGTGTTGTGCGTTTCTGGCAATGGTTACCCCTTTTCG 900  
 110 I Y F L T V L S V V R F L A M V H P F R 129

Figure 1B

901 GCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCT 960  
 130 L L H V T S I R S A W I L C G I I W I L 149  
  
 961 TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTAC 1020  
 150 I M A S S I M L L D S G S E Q N G S V T 169  
  
 1021 ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGC 1080  
 170 S C L E L N L Y K I A K L Q T M N Y I A 189  
  
 1081 CTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCAT 1140  
 190 L V V G C L L P F F T L S I C Y L L I I 209  
  
 1141 TCGGGTTCTGTAAAGTGGAGGTCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGC 1200  
 210 R V L L K V E V P E S G L R V S H R K A 229  
  
 1201 ACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTTTCTGCCCCTATCACAC 1260  
 230 L T T I I I T L I I F F L C F L P Y H T 249  
  
 1261 ACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAA 1320  
 250 L R T V H L T T W K V G L C K D R L H K 269  
  
 1321 AGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTA 1380  
 270 A L V I T L A L A A A N A C F N P L L Y 289  
  
 1381 TTACTTTGCTGGGAGAAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC 1440  
 290 Y F A G E N F K D R L K S A L R K G H P 309  
  
 1441 ACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAG 1500  
 310 Q K A K T K C V F P V S V W L R K E T R 329  
  
 1501 AGTATAAGGAGCTCTTAGATGAGACCTGTTCTTGTATCCTTGTGTCCATCTTCATTCAC 1560  
 330 V \* 331  
  
 1561 CATAGTCTCCAAATGACTTTGTATTTACATCACTCCCAACAAATGTTGATTCTTAATATT 1620  
  
 1621 TAGTTGACCATTACTTTTGTTAATAAGACCTACTTCAAAAATTTTATTCAAGTGTAACAAA 1680  
  
 1681 AAAAAAAAAAAAAAAAAAAAAAAAAA 1708

Figure 2A

		1		50
HGPRBMY11	(1)	-----MSLQPSISVSEMEPN-----TFSNNNSRNCITEN--FK		
HGPRBMY11v1	(1)	MERKFMSLQPSISVSEMEPN-----TFSNNNSRNCITEN--FK		
P2Y5_CHICK	(1)	-----MVSSNCSTEDS--FK		
P2YR_CHICK	(1)	MTEALISAALNGTQPELLAGG-----WAAGNATKCSITKIGFO		
P2YR_MELGA	(1)	MTEALISAALNGTQPELLAGG-----WAAGNATKCSITKIGFO		
P2YR_RAT	(1)	MTEVPWSAVPNGTDAFLAGLGLSLWGNSTIASIAAVSSSFRCAIITKIGFO		
Q9Y271	(1)	-----MDETG-----NLTVSSATCHDTIDDER		
GPRH_HUMAN	(1)	-----MNGLEVAPP-----LITNFSLATAEQCGQETPEE		
		51		100
HGPRBMY11	(22)	REEFFPIVYLLIFFWGVLGNGLSIVFLOPYKKSTSVNVFMENLAISDLIE		
HGPRBMY11v1	(38)	REEFFPIVYLLIFFWGVLGNGLSIVFLOPYKKSTSVNVFMENLAISDLIE		
P2Y5_CHICK	(14)	YTLGCVFESMVFLGLTANCAVAIYIFITLKVNRNETTITMENLAISDLIE		
P2YR_CHICK	(40)	FYYLPTVYILVFIITGFLGNSVAIWMFVTHMRPWSGISVYFMENLALADELY		
P2YR_MELGA	(40)	FYYLPTVYILVFIITGFLGNSVAIWMFVTHMRPWSGISVYFMENLALADELY		
P2YR_RAT	(51)	FYYLPAVYILVFIITGFLGNSVAIWMFVTHMRPWSGISVYFMENLALADELY		
Q9Y271	(23)	NQVYSTLYSMISVVGFEFGNFVAVLTKTYHKKSATFOVYMINLAVADLLIC		
GPRH_HUMAN	(31)	NMLEASFYLLDFILALVGNITLALWLETRDHKSGTPANVEIMHLAVADLSC		
		101		150
HGPRBMY11	(72)	ISTLPFRADYVLRGSNWIFGDLACRIMSYSILYVMYSSIIYELTVLSVVR		
HGPRBMY11v1	(88)	ISTLPFRADYVLRGSNWIFGDLACRIMSYSILYVMYSSIIYELTVLSVVR		
P2Y5_CHICK	(64)	VETLPFRILYFVVRN--WPEGDVICKISVTIFYINMYGSILFLTCSVDRF		
P2YR_CHICK	(90)	VLTLPALIFYENKTDWIFGDVMCKLQREIFHVNLYGSILFLTCSVHRY		
P2YR_MELGA	(90)	VLTLPALIFYENKTDWIFGDVMCKLQREIFHVNLYGSILFLTCSVHRY		
P2YR_RAT	(101)	VLTLPALIFYENKTDWIFGDVMCKLQREIFHVNLYGSILFLTCSAHRY		
Q9Y271	(73)	VCTLPRLRVVYVHKGIFLQDFLCRLSTYALYVNLVCSIFFMTAMSFRC		
GPRH_HUMAN	(81)	VLVLPTRLVYHISGNHWPFGETACRLTGEFLYLNMYASTIYELTCSADRF		
		151		200
HGPRBMY11	(122)	LAMVHPERLHVTISIRSAWILCGTIWILIMASSIMILDS---GSEONGSV		
HGPRBMY11v1	(138)	LAMVHPERLHVTISIRSAWILCGTIWILIMASSIMILDS---GSEONGSV		
P2Y5_CHICK	(113)	LAIVHPEFSKTLRTKRNARIVCVAVWITVLAGSTPASEFQSTNRQNTEQ		
P2YR_CHICK	(140)	TGVVHPLKSLGRLKKKNNAVYVSSLVWALVVAVIAPILFYSGTGVRNRKTI		
P2YR_MELGA	(140)	TGVVHPLKSLGRLKKKNNAVYVSSLVWALVVAVIAPILFYSGTGVRNRKTI		
P2YR_RAT	(151)	SGVVHPLKSLGRLKKKNNAVYVSVLVVLIIVVAISPILFYSGTGIRKNKTV		
Q9Y271	(123)	IATVPEVONINLVTKKARFVCGIWIIFVILTSSPFLMAKPQKDEKNNTK		
GPRH_HUMAN	(131)	LAIVHPEVKSILKLRRLPYAHLACAFLLVVVAVAMAPLLVSPQTVQTNHTVV		
		201		250
HGPRBMY11	(169)	TSCLE--LNLYKIAKLQTMNYIALVVGCLIPFETLSICYLLIIRVILKVE		
HGPRBMY11v1	(185)	TSCLE--LNLYKIAKLQTMNYIALVVGCLIPFETLSICYLLIIRVILKVE		
P2Y5_CHICK	(163)	RTCFENFPESTWKTYLSRIVIFIEIVGFFIPLILNVTCTMTVIRTNKPL		
P2YR_CHICK	(190)	TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALTYKD		
P2YR_MELGA	(190)	TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALTYKD		
P2YR_RAT	(201)	TCYDS--TSDEYLRSYFIYSMCTTVAMFCIPLVLILGCYGLIVRALTYKD		
Q9Y271	(173)	CFEPP--QDNQTKNHVLVLHYVSLFVGFIIPFVIIIVCYTMIILTLKKS		
GPRH_HUMAN	(181)	CLQLY-----REKASHHALVSLAVAFTFPFIITTVTCYLLIIRSLRQGL		

Figure 2B

		251		300
HGPRBMY11	(217)	VPESGLRVSHRKALTTIIITLIIFFFLCFLPYHTLRTVHL	-----	TIWKV
HGPRBMY11v1	(233)	VPESGLRVSHRKALTTIIITLIIFFFLCFLPYHTLRTVHL	-----	TIWKV
P2Y5_CHICK	(213)	TLSRNKLS-KKKVLKMTFVHIVIECFCEVPYNITLIIYSLMR	--	TOIWIN
P2YR_CHICK	(238)	LDNSPLR---RKSTYLVIIVLTVFAVSYPFHVMKTLNLRARLDFOTPM		
P2YR_MELGA	(238)	LDNSPLR---RKSTYLVIIVLTVFAVSYPFHVMKTLNLRARLDFOTPM		
P2YR_RAT	(249)	LDNSPLR---RKSTYLVIIVLTVFAVSYPFHVMKTMNLRARLDFOTPEM		
Q9Y271	(221)	MKKNLSS--HKKAIGMTMVTAALVSEMPYHIQRTIHLHFLHN	--	ETKP
GPRH_HUMAN	(224)	RVEKRLK---TKAVRMIAIVLALFLVCFVPYHVNRSVYVLHYR	--	SHGAS
		301		350
HGPRBMY11	(261)	GLCKDRLHKALVITIALAANACENPLLYYFAGENFKDRLKSALRK		GHPO
HGPRBMY11v1	(277)	GLCKDRLHKALVITIALAANACENPLLYYFAGENFKDRLKSALRK		GHPO
P2Y5_CHICK	(260)	CSVVTAVRTMYPVITLCTAVSNCCFDPIVYYFTSDINSELDK	--	KQQ--VH
P2YR_CHICK	(285)	CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR		
P2YR_MELGA	(285)	CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR		
P2YR_RAT	(296)	CDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKASRR		
Q9Y271	(267)	CDSVLRMQKSVVITLSLASNCCFDPLLYFFSGGNFRKRLS		TFRKHSLS
GPRH_HUMAN	(269)	CATQRILALANRITSCLTSLNGALDPIMYFFFAEKFRHALCNLLCGKRLK		
		351		379
HGPRBMY11	(311)	KAK-TKCVFPVSVWLKKEIRV	-----	
HGPRBMY11v1	(327)	KAK-TKCVFPVSVWLKKEIRV	-----	
P2Y5_CHICK	(306)	QNT	-----	
P2YR_CHICK	(335)	SEP-NVQSKSEEMTLNILEYKONGDTSL		
P2YR_MELGA	(335)	SEP-NVQSKSEEMTLNILEYKONGDTSL		
P2YR_RAT	(346)	SEA-NLQSKSEEMTLNILEYKONGDTSL		
Q9Y271	(316)	SVT-YVPRKKASLPEKGEEICRV	-----	
GPRH_HUMAN	(319)	GPPPSFEGKTNESSSAKSEL	-----	

Figure 3

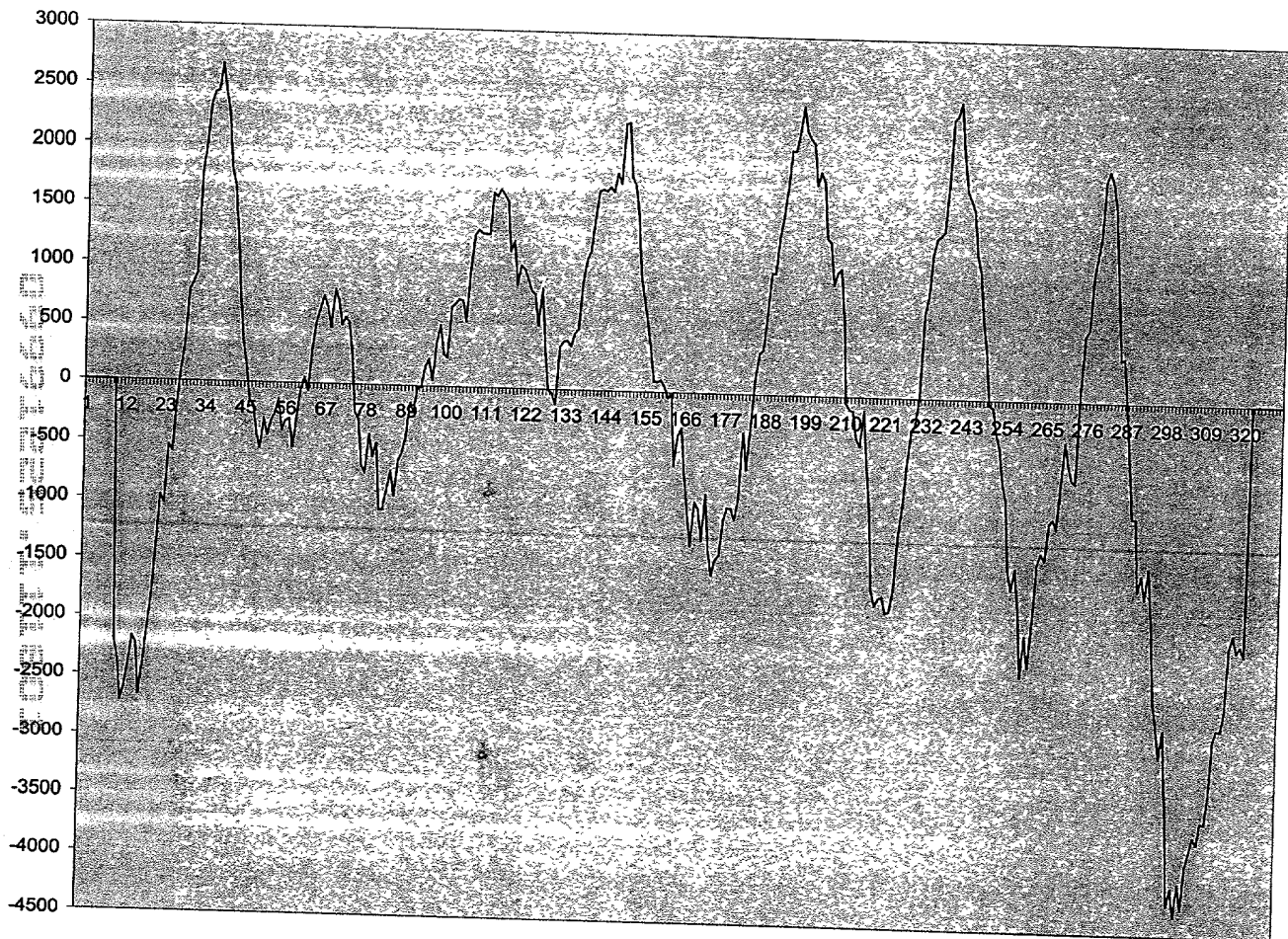


Figure 4.

## Expression Profiling of Novel Human GPCR, HGPRBMY11

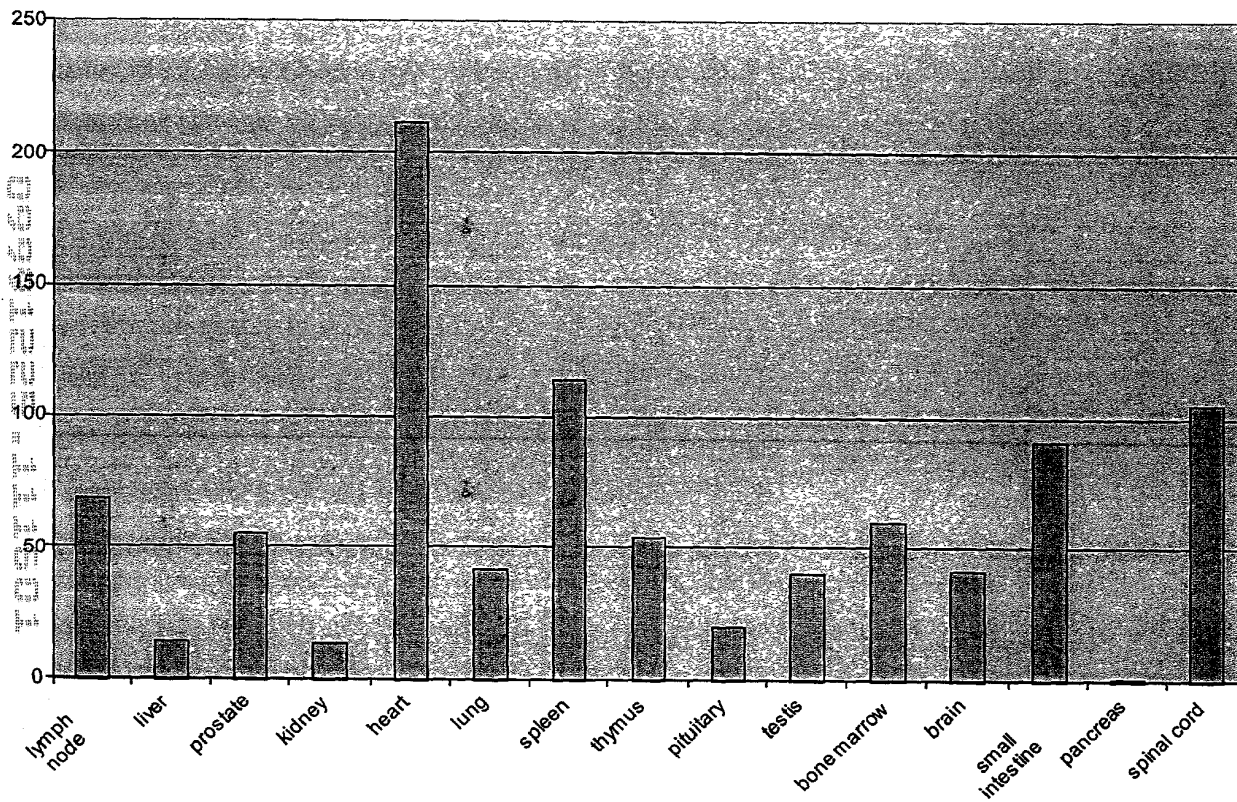


Figure 5.

## HGPRBMY11

Protein	Genbank ID	Identities	Similarities
human cysteinyl leukotriene receptor	gi 11422069	37%	49%
chick purinergic receptor 5	gi P32250	36%	46%
human G-protein-coupled receptor GPR17	gi Q13304	36%	46%
chick purinergic receptor	gi P34996	30%	45%
turkey purinergic receptor	gi P49652	30%	45%
rat purinergic receptor	gi P49651	30%	44%

## HGPRBMY11v1

Protein	Genbank ID	Identities	Similarities
human cysteinyl leukotriene receptor	gi 11422069	37.2%	49%
chick purinergic receptor 5	gi P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi Q13304	36.2%	46.1%
chick purinergic receptor	gi P34996	29.5%	43.9%
turkey purinergic receptor	gi P49652	29.8%	44.2%
rat purinergic receptor	gi P49651	29.6%	44%

Figure 6A

1	ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT	60
1	M E R K F M S L Q P S I S V S E M E P N	20
61	GGCACCTTCAGCAATAACAACAGCAGGAACGCACAATTGAAAACCTTCAAGAGAGAATTT	120
21	G T F S N N N S R N C T I E N F K R E <u>F</u>	40
121	TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA	180
41	<u>F P I V Y L I I F F W G V L G N G L S I</u>	60
181	TATGTTTTCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTG	240
61	<u>Y V F L</u> Q P Y K K S T S V N <u>V F M L N L</u>	80
241	GCCATTTTCAGATCTCCTGTTCATAAGCAGCCTTCCCTTCAGGGCTGACTATTATCTTAGA	300
81	<u>A I S D L L F I S T L P F R A D Y Y L R</u>	100
301	GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC	360
101	G S N W I F G D L A C R I M S Y S L Y <u>V</u>	120
361	AACATGTACAGCAGTATTTATTTCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATG	420
121	<u>N M Y S S I Y F L T V L S V V R F L A M</u>	140
421	GTTCAACCCCTTTTCGGCTTCTGCATGTACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG	480
141	<u>V H P F R L L H V T S I R S</u> <u>A W I L C G</u>	160
481	ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG	540
161	<u>I I W I L I M A S S I M L L</u> D S G S E Q	180
541	AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC	600
181	N G S V T S C L E L N L Y K <u>I A K L Q T</u>	200
601	ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT	660
201	<u>M N Y I A L V V G C L L P F F T L S I C</u>	220
661	TATCTGCTGATCATTCGGGTCTGTAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT	720
221	<u>Y L L I I R V L L K V E V P E S G L R V</u>	240
721	TCTCACAGGAAGGCACTGACCACCATCATCATCCTTGATCATCTTCTTCTTGTGTTTC	780
241	S H R K <u>A L T T I I I T L I I F F L C F</u>	260
781	CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAA	840
261	<u>L P Y H T L</u> R T V H L T T W K V G L C K	280
841	GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC	900
281	D R L H K <u>A L V I T L A L A A A N A C F</u>	300



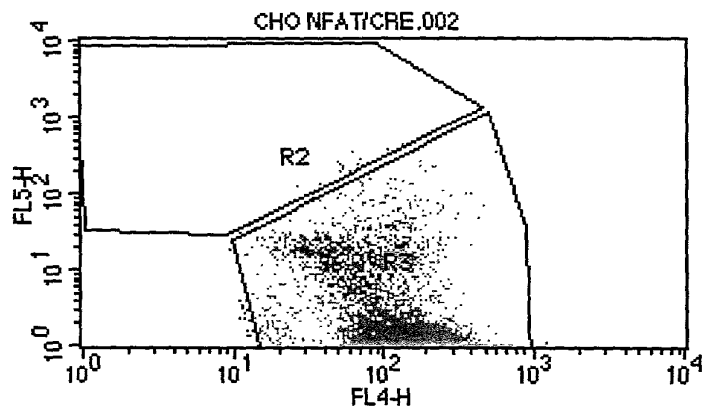
Figure 6B

901 AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTC 960  
301 N P L L Y Y F A G E N F K D R L K S A L 320

961 AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTG 1020  
321 R K G H P Q K A K T K C V F P V S V W L 340

1021 AGAAAGGAAACAAGAGTATAA 1041  
341 R K E T R V 346

Figure 7



00075 NP

Figure 8

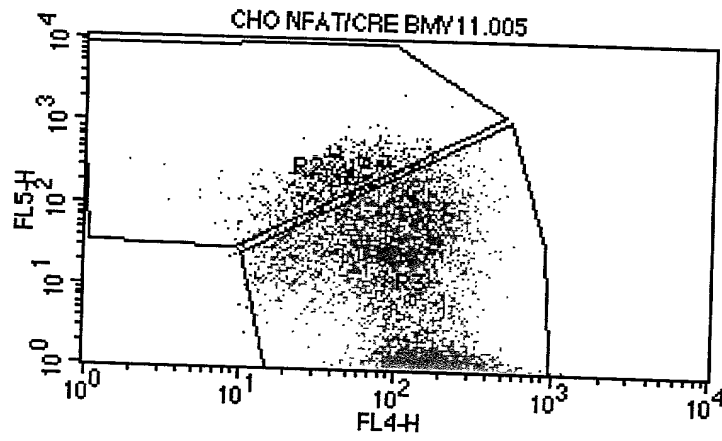




Figure 10

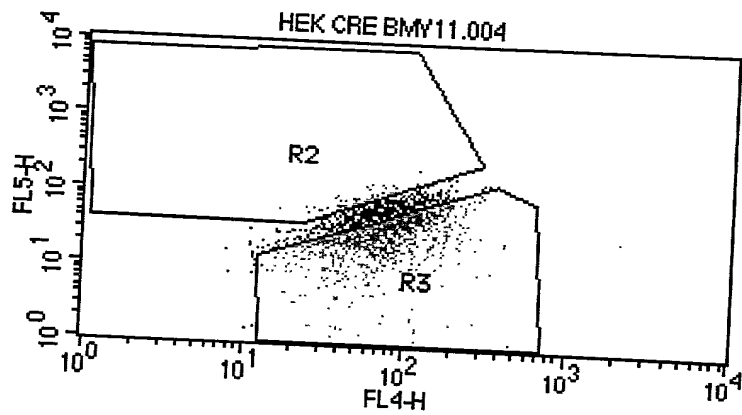


Figure 11

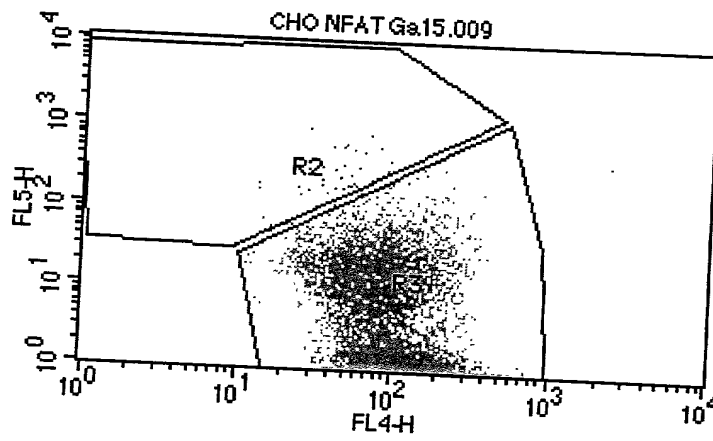
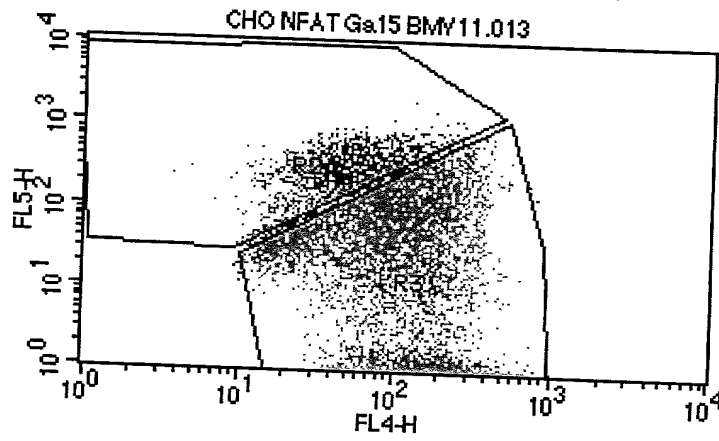
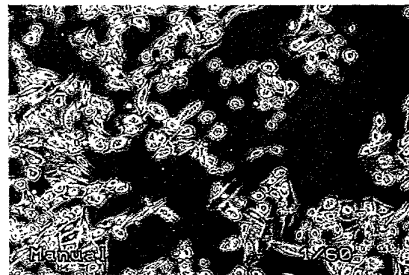


Figure 12



**Figure 13**

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)



Cho NFAT Ga15 BMY11 (Fluorescent vs. Bright Field)

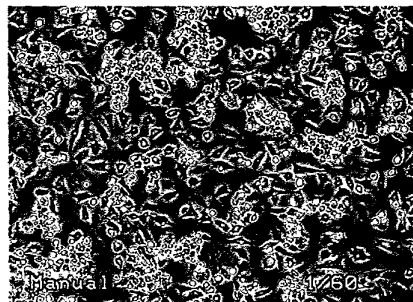
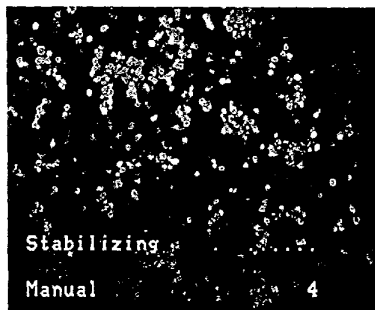
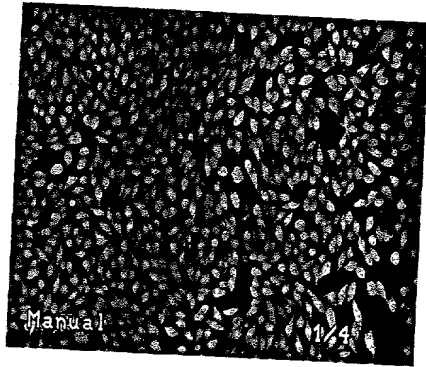


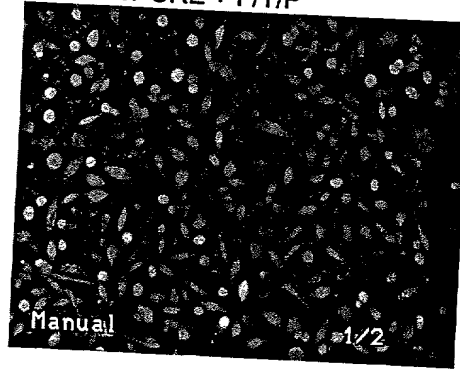


Figure 14

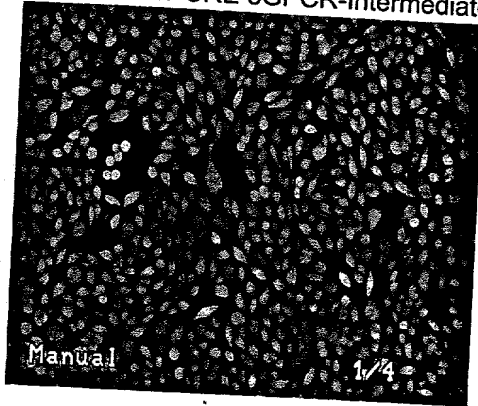
a. Cho-NFAT CRE



b. Cho-NFAT CRE + F/T/P



c. Cho-NFAT CRE oGPCR-Intermediate



d. Cho-NFAT CRE oGPCR High



Figure 15A

1	ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT	60
1	M S L Q P S I S V S E M E P N G T F S N	20
61	AACAACAGCAGGAACTGCACAATTGAAAACCTCAAGAGAGAATTTTCCCAATTGTATAT	120
21	N N S R N C T I E N F K R E F F P I V Y	40
121	CTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCTGCAG	180
41	L I I F F W G V L G N G L S I Y V F L Q	60
181	CCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTGGCCATTTTCAGATCTC	240
61	P Y K K S T S V N V F M L N L A I S D L	80
241	CTGTTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA	300
81	L F I S T L P F R A D Y Y L R G S N W I	100
301	TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGT	360
101	F G D L A C R I M S Y S L Y V N M Y S S	120
361	ATTTATTTCTGACCGTGTGAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTTCGG	420
121	I Y F L T V L S V V R F L A M V H P F R	140
421	CTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT	480
141	L L H V T S I R S A W I L C G I I W I L	160
481	ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCA	540
161	I M A S S I M L L D S G S E Q N G S V T	180
541	TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGCC	600
181	S C L E L N L Y K I A K L Q T M N Y I A	200
601	TTGGTGGTGGGCTGCCTGCTGCCATTTTTACACTCAGCATCTGTTATCTGCTGATCATT	660
201	L V V G C L L P F F T L S I C Y L L I I	220
661	CGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA	720
221	R V L L K V E V P E S G L R V S H R K A	240
721	CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCTGCCCTATCACACA	780
241	L T T I I I T L I I F F L C F L P Y H T	260
781	CTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA	840
261	L R T V H L T T W K V G L C K D R L H K	280
841	GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT	900
281	A L V I T L A L A A A N A C F N P L L Y	300

Figure 15B

901 TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA 960  
301 Y F A G E N F K D R L K S A L R K G H P 320

961 CAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAGA 1020  
321 Q K A K T K C V F P V S V W L R K E T R 340

1021 GTATAA 1026  
341 V 341

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